

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/578,840
Source: PG
Date Processed by STIC: 5/22/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**> , **EFS Submission User Manual - ePAVE**)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):**
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06



IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/578,840

DATE: 05/22/2006

TIME: 14:19:19

Input Set : A:\060641-0113sequencetext.txt

Output Set: N:\CRF4\05222006\J578840.raw

2 <110> APPLICANT: Chugai Seiyaku Kabushiki Kaisha
W--> 3 <120> TITLE OF INVENTION: Humanized anti-CD47 antibody
W--> 4 <130> FILE REFERENCE: YCT-971
C--> 5 <140> CURRENT APPLICATION NUMBER: US/10/578,840
C--> 5 <141> CURRENT FILING DATE: 2006-05-10
W--> 5 <160> NUMBER OF SEQ ID: 92

ERRORED SEQUENCES

441 <210> SEQ ID NO: 32
442 <211> LENGTH: 130
443 <212> TYPE: DNA
444 <213> ORGANISM: Artificial Sequence
W--> 445 <220> FEATURE:
W--> 446 <223> OTHER INFORMATION:
E--> 446 <400> SEQUENCE: (130) 32 (change to)
447 cagcagagggc caggccaatc tccaaggcgc ctaatttata aagtttccaa ccgattttct 60
448 ggtgtcccag acagattcag cggcagtgagg tcaggcactg atttcacact gaaaatcagc 120
449 aggggtggagg 130
471 <210> SEQ ID NO: 35
472 <211> LENGTH: (23) 22 ← shown below
473 <212> TYPE: DNA
474 <213> ORGANISM: Artificial Sequence
W--> 475 <220> FEATURE:
W--> 476 <223> OTHER INFORMATION:
E--> 476 <400> SEQUENCE: (23) 35 ← same error as above
E--> 477 ccaagcttc caccatgagg ctc (23) 22
479 <210> SEQ ID NO: 36
480 <211> LENGTH: 23
481 <212> TYPE: DNA
482 <213> ORGANISM: Artificial Sequence
W--> 483 <220> FEATURE:
W--> 484 <223> OTHER INFORMATION:
E--> 484 <400> SEQUENCE: (23) 36 ←
485 cgcggatcca ctcacgtttg atc 23
487 <210> SEQ ID NO: 37
488 <211> LENGTH: 412
E--> 489 (212) ← insert these mandatory numeric identifiers and
E--> 490 (213) responder
W--> 491 <400> SEQUENCE: 37
492 atg agg ctc cct gct cag ctc ctg ggg ctg cta atg ctc tgg gtc cca 48
493 Met Arg Leu Pro Ala Gln Leu Leu Gly Leu Leu Met Leu Trp Val Pro

-20

-15

-10

-5

insert these amino acid numbers

see pp 1-8
Suggestion: Consult
Sequence Rules
for valid format

Does Not Comply
Corrected Diskette Needed

(global error)

see p. 7 for error

exploration

↓
This error appears in many sequences

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Input Set : A:\060641-0113sequencetext.txt

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```

495 ggc tcc agt ggg gat gtt gtg atg act cag tct cca ctc tcc ctg ccc 96
496 Gly Ser Ser Gly Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro
497      -1 1      5      10
498 gtc acc ctt gga cag ccg gcc tcc atc tcc tgc aga tca agt cag agc 144
499 Val Thr Leu Gly Gln Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
500      15      20      25
501 ctt gtg cac agt aat gga aag acc tat tta cat tgg ttt cag cag agg 192
502 Leu Val His Ser Asn Gly Lys Thr Tyr Leu His Trp Phe Gln Gln Arg
503      30      35      40
504 cca ggc caa tct cca agg cgc cta att tat aaa gtt tcc aac cga ttt 240
505 Pro Gly Gln Ser Pro Arg Arg Leu Ile Tyr Lys Val Ser Asn Arg Phe
506      45      50      55      60
507 tct ggt gtc cca gac aga ttc agc ggc agt ggg tca ggc act gat ttc 288
508 Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
509      65      70      75
510 aca ctg aaa atc agc agg gtg gag gct gag gat gtt gga gtt tat tac 336
511 Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr
512      80      85      90
513 tgc tct caa agt aca cat gtt ccg tac acg ttt ggc cag ggg acc aag 384
514 Cys Ser Gln Ser Thr His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys
515      95      100      105
516 ctg gag atc aaa cgt gag tgg atc cgc g 412
517 Leu Glu Ile Lys
518      110

```

773 <210> SEQ ID NO: 54

774 <211> LENGTH: 39

775 <212> TYPE: DNA

776 <213> ORGANISM: Artificial Sequence

W--> 777 <220> FEATURE:

W--> 778 <223> OTHER INFORMATION:

E--> 778 <400> SEQUENCE: ⑤ 54 ←

779 ggggtggaggc tgatgatgtt ggaatttatt actgctctc 39

960 <210> SEQ ID NO: 68

961 <211> LENGTH: ②④ 25 shown

962 <212> TYPE: DNA

963 <213> ORGANISM: Artificial Sequence

W--> 964 <220> FEATURE:

W--> 965 <223> OTHER INFORMATION:

W--> 965 <400> SEQUENCE: 68

E--> 966 aggtgtcgac tcccaggtgc agctg ②④ 25

984 <210> SEQ ID NO: 71

985 <211> LENGTH: ④⑤ 46

986 <212> TYPE: DNA

987 <213> ORGANISM: Artificial Sequence

W--> 988 <220> FEATURE:

W--> 989 <223> OTHER INFORMATION:

W--> 989 <400> SEQUENCE: 71

E--> 990 aaaaggaaaa gcggccgctc attatttgat ctccagcttg gtcccc ④⑤ 46

992 <210> SEQ ID NO: 72

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/578,840

DATE: 05/22/2006

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Input Set : A:\060641-0113sequencetext.txt

Output Set: N:\CRF4\05222006\J578840.raw

```

993 <211> LENGTH: 15
994 <212> TYPE: DNA
E--> 995 <213> ← insert mandatory response
W--> 996 <400> SEQUENCE: 72
997 ggt ggc gga ggt tcc 15
998 Gly Gly Gly Gly Ser
999 1 5
1125 <210> SEQ ID NO: 77
1126 <211> LENGTH: 45
1127 <212> TYPE: DNA
E--> 1128 <213> ← insert mandatory response
W--> 1129 <400> SEQUENCE: 77
1130 ggt ggt ggt ggt tcc ggt ggt ggt gga tcc ggt ggt ggc gga tcc 45
1131 Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser
1132 1 5 10 15
1395 <210> SEQ ID NO: 87
1396 <211> LENGTH: 36
1397 <212> TYPE: DNA
1398 <213> ORGANISM: Artificial Sequence
W--> 1399 <220> FEATURE:
W--> 1400 <223> OTHER INFORMATION:
W--> 1400 <400> SEQUENCE: 87
E--> 1401 gggcagtgcc caagactcct gatctacaaa gtttcc 36 ← insert
1403 <210> SEQ ID NO: 88
1404 <211> LENGTH: 37
1405 <212> TYPE: DNA
1406 <213> ORGANISM: Artificial Sequence
W--> 1407 <220> FEATURE:
W--> 1408 <223> OTHER INFORMATION:
W--> 1408 <400> SEQUENCE: 88
E--> 1409 tcattatttg atctcaagct tgggtcccctg gccaaac 37 ←
1412 <210> SEQ ID NO: 89
1413 <211> LENGTH: 708
1414 <212> TYPE: DNA
E--> 1415 <213> ← insert mandatory response
W--> 1416 <400> SEQUENCE: 89
1417 caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgcaggtt 60
1418 tcctgtaagg catctggata caccttcacc aaccatgtta ttcactggct gcgacaggcc 120
1419 cccgggcaat gccttgagtg gatgggatat atttatcctt acaatgatgg tactaagtat 180
1420 aatgagaagt tcaaggacag agtcacgatg acctcagaca cgtccatcag cacagcctac 240
1421 atggagttga gcagtctcag atctgacgac acggccgtct attattgtgc tagaggggggt 300
1422 tactatactt acgacgactg gggccaagca accctggcca cagtctcgag tgggtggcgga 360
1423 ggttccgata ttgtgatgac tcagtctcca ctctccctgc ccgtcacccc tggagagccg 420
1424 gcctccatct cctgcagatc aagtcagagc cttgtgcaca gtaatggaaa gacctattta 480
1425 catttggtatc tgcagaagcc aggccagtct ccaagactcc tgatctacaa agtttccaac 540
1426 cgatttttctg gtgtcccaga cagattcagc ggcagtggtt caggcactga tttcacactg 600
1427 aaaatcagca ggggtggaggc tgatgatgtt ggaatttatt actgctctca aagtacacat 660
E--> 1428 gttccgtaca cgtttggtcg cgggaccaag cttgagatca aataatga 708 ←
1430 <210> SEQ ID NO: 90

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/578,840

DATE: 05/22/2006

TIME: 14:19:20

Input Set : A:\060641-0113sequencetext.txt

Output Set: N:\CRF4\05222006\J578840.raw

1431 <211> LENGTH: 234

1432 <212> TYPE: PRT

E--> 1433 <213> *Insert mandatory response*

W--> 1434 <400> SEQUENCE: 90

1435 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
 1436 1 5 10 15
 1437 Ser Val Gln Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn His
 1438 20 25 30
 1439 Val Ile His Trp Leu Arg Gln Ala Pro Gly Gln Cys Leu Glu Trp Met
 1440 35 40 45
 1441 Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe
 1442 50 55 60
 1443 Lys Asp Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
 1444 65 70 75 80
 1445 Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
 1446 85 90 95
 1447 Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln Ala Thr Leu
 1448 100 105 110
 1449 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln
 1450 115 120 125
 1451 Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser
 1452 130 135 140
 1453 Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu
 1454 145 150 155 160
 1455 His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Arg Leu Leu Ile Tyr
 1456 165 170 175
 1457 Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
 1458 180 185 190
 1459 Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Asp
 1460 195 200 205
 1461 Asp Val Gly Ile Tyr Tyr Cys Ser Gln Ser Thr His Val Pro Tyr Thr
 1462 210 215 220
 1463 Phe Gly Cys Gly Thr Lys Leu Glu Ile Lys
 1464 225 230

1466 <210> SEQ ID NO: 91

1467 <211> LENGTH: 708

1468 <212> TYPE: DNA

E--> 1469 <213> *Insert mandatory response*

W--> 1470 <400> SEQUENCE: 91

1471 caggtgcagc tgggtgcagtc tggggctgag gtgaagaagc ctggggcctc agtgcaggtt 60
 1472 tcctgtaagg catctggata caccttcacc aaccatgtta ttactggct gcgacaggcc 120
 1473 cctgggcaag ggcttgagtg gatgggatat atttatcctt acaatgatgg tactaagtat 180
 1474 aatgagaagt tcaaggacag agtcacgatg acctcagaca cgtccatcag cacagcctac 240
 1475 atggagttga gcagtctcag atctgacgac acggccgtat actattgtgc tagaggggggt 300
 1476 tactatactt acgacgactg gggctgcgca accctgggtca cagtctcgag tgggtggcgga 360
 1477 ggttccgata ttgtgatgac tcagtctcca ctctccctgc ccgtcacccc tggagagccg 420
 1478 gcctccatct cctgcagatc aagtcagagc cttgtgcaca gtaatggaaa gacctattta 480
 1479 cattggtatc tgcagaagcc cgggcagtgc ccaagactcc tgatctacaa agtttccaac 540
 1480 cgattttctg gtgtcccaga cagattcagc ggcagtgggt caggcactga tttcacactg 600

RAW SEQUENCE LISTING

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Input Set : A:\060641-0113sequencetext.txt

Output Set: N:\CRF4\05222006\J578840.raw

1481 aaaatcagca ggggtggaggc tgatgatggtt ggaatttatt actgctctca aagtacacat 660
E--> 1482 gttccgtaca cgtttggcca ggggaccaag cttgagatca aataatga 708 ← insert
1484 <210> SEQ ID NO: 92
1485 <211> LENGTH: 234
1486 <212> TYPE: PRT
E--> 1487 <213> *insert mandatory response*
W--> 1488 <400> SEQUENCE: 92
1489 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
1490 5 10 15
1491 Ser Val Gln Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn His
1492 20 25 30
1493 Val Ile His Trp Leu Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
1494 35 40 45
1495 Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn Glu Lys Phe
1496 50 55 60
1497 Lys Asp Arg Val Thr Met Thr Ser Asp Thr Ser Ile Ser Thr Ala Tyr
1498 65 70 75 80
1499 Met Glu Leu Ser Ser Leu Arg Ser Asp Asp Thr Ala Val Tyr Tyr Cys
1500 85 90 95
1501 Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Cys Ala Thr Leu
1502 100 105 110
1503 Val Thr Val Ser Ser Gly Gly Gly Gly Ser Asp Ile Val Met Thr Gln
1504 115 120 125
1505 Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu Pro Ala Ser Ile Ser
1506 130 135 140
1507 Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Lys Thr Tyr Leu
1508 145 150 155 160
1509 His Trp Tyr Leu Gln Lys Pro Gly Gln Cys Pro Arg Leu Leu Ile Tyr
1510 165 170 175
1511 Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser
1512 180 185 190
1513 Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Asp
1514 195 200 205
1515 Asp Val Gly Ile Tyr Tyr Cys Ser Gln Ser Thr His Val Pro Tyr Thr
1516 210 215 220
1517 Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
1518 225 230
E--> 1523 ① *delete*

10/578,840 6

<210> 7
 <211> 424
 <212> DNA
 <213> Mouse, Human
 <400> 7

atg gaa tgg agc tgg ata ttt ctc ttc ctc ctg tca gga act gca ggt 48
 Met Glu Trp Ser Trp Ile Phe Leu Phe Leu Leu Ser Gly Thr Ala Gly
 gtc cac tcc cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag 96
 Val His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys
 -1 1 5 10

← insert
 these
 numbers

same error in sequence 10, seq. 13, 16, 19,
 22, 30, 40, 43, 46,
 49, 52, 57, 64, 67, 73,
 74, 78, 79,

7

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/578,840

DATE: 05/22/2006
TIME: 14:19:21

error explanation Input Set : A:\060641-0113sequencetext.txt
Output Set: N:\CRF4\05222006\J578840.raw

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223>

section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32)

(Sec.1.823 of new Rules)

Seq#:1,2,3,4,5,6,8,9,11,12,14,15,17,18,20,21,23,24,25,26,27,28,29,31,32,33,34

Seq#:35,36,38,39,41,42,44,45,47,48,50,51,53,54,55,56,58,59,60,61,62,63,65,66

Seq#:68,69,70,71,75,76,80,81,82,83,84,85,86,87,88

delete brackets

10/578,840

8

(Sequence Listing)

<110> Chugai Seiyaku Kabushiki Kaisha

VERIFICATION SUMMARY

DATE: 05/22/2006

PATENT APPLICATION: US/10/578,840

TIME: 14:19:21

Input Set : A:\060641-0113sequencetext.txt

Output Set: N:\CRF4\05222006\J578840.raw

L:3 M:283 W: Missing Blank Line separator, <120> field identifier
L:4 M:283 W: Missing Blank Line separator, <130> field identifier
L:5 M:270 C: Current Application Number differs, Replaced Current Application No
L:5 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:5 M:283 W: Missing Blank Line separator, <160> field identifier
L:11 M:283 W: Missing Blank Line separator, <220> field identifier
L:12 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:1, <213>
ORGANISM:Artificial Sequence
L:12 M:283 W: Missing Blank Line separator, <400> field identifier
L:12 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:12
L:21 M:283 W: Missing Blank Line separator, <220> field identifier
L:22 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:Artificial Sequence
L:22 M:283 W: Missing Blank Line separator, <400> field identifier
L:22 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:22
L:31 M:283 W: Missing Blank Line separator, <220> field identifier
L:32 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:3, <213>
ORGANISM:Artificial Sequence
L:32 M:283 W: Missing Blank Line separator, <400> field identifier
L:32 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:32
L:41 M:283 W: Missing Blank Line separator, <220> field identifier
L:42 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:Artificial Sequence
L:42 M:283 W: Missing Blank Line separator, <400> field identifier
L:42 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:42
L:51 M:283 W: Missing Blank Line separator, <220> field identifier
L:52 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>
ORGANISM:Artificial Sequence
L:52 M:283 W: Missing Blank Line separator, <400> field identifier
L:52 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:52
L:59 M:283 W: Missing Blank Line separator, <220> field identifier
L:60 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Artificial Sequence
L:60 M:283 W: Missing Blank Line separator, <400> field identifier
L:60 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:60
L:67 M:283 W: Missing Blank Line separator, <400> field identifier
L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:73 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:100 M:283 W: Missing Blank Line separator, <220> field identifier
L:101 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Artificial Sequence
L:101 M:283 W: Missing Blank Line separator, <400> field identifier
L:101 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8,Line#:101
L:108 M:283 W: Missing Blank Line separator, <220> field identifier
L:109 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:9, <213>
ORGANISM:Artificial Sequence
L:109 M:283 W: Missing Blank Line separator, <400> field identifier
L:109 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:109
L:116 M:283 W: Missing Blank Line separator, <400> field identifier
L:120 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:122 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:149 M:283 W: Missing Blank Line separator, <220> field identifier
L:150 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:11, <213>

ORGANISM:Artificial Sequence

L:150 M:283 W: Missing Blank Line separator, <400> field identifier

L:150 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:11,Line#:150

L:157 M:283 W: Missing Blank Line separator, <220> field identifier

VERIFICATION SUMMARY

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TIME: 14:19:21

Input Set : A:\060641-0113sequencetext.txt

Output Set: N:\CRF4\05222006\J578840.raw

L:158 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>
ORGANISM:Artificial Sequence
L:158 M:283 W: Missing Blank Line separator, <400> field identifier
L:158 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12,Line#:158
L:165 M:283 W: Missing Blank Line separator, <400> field identifier
L:169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:13
L:198 M:283 W: Missing Blank Line separator, <220> field identifier
L:199 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:14, <213>
ORGANISM:Artificial Sequence
L:199 M:283 W: Missing Blank Line separator, <400> field identifier
L:199 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:14,Line#:199
L:206 M:283 W: Missing Blank Line separator, <220> field identifier
L:207 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:15, <213>
ORGANISM:Artificial Sequence
L:207 M:283 W: Missing Blank Line separator, <400> field identifier
L:207 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:207
L:214 M:283 W: Missing Blank Line separator, <400> field identifier
L:218 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:220 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:16
L:247 M:283 W: Missing Blank Line separator, <220> field identifier
L:248 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:17, <213>
ORGANISM:Artificial Sequence
L:248 M:283 W: Missing Blank Line separator, <400> field identifier
L:248 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:17,Line#:248
L:255 M:283 W: Missing Blank Line separator, <220> field identifier
L:256 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:18, <213>
ORGANISM:Artificial Sequence
L:256 M:283 W: Missing Blank Line separator, <400> field identifier
L:256 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:18,Line#:256
L:263 M:283 W: Missing Blank Line separator, <400> field identifier
L:267 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:269 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19
L:296 M:283 W: Missing Blank Line separator, <220> field identifier
L:297 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:20, <213>
ORGANISM:Artificial Sequence
L:297 M:283 W: Missing Blank Line separator, <400> field identifier
L:297 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20,Line#:297
L:304 M:283 W: Missing Blank Line separator, <220> field identifier
L:305 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:21, <213>
ORGANISM:Artificial Sequence
L:305 M:283 W: Missing Blank Line separator, <400> field identifier
L:305 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:21,Line#:305
L:312 M:283 W: Missing Blank Line separator, <400> field identifier
L:316 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:318 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:346 M:283 W: Missing Blank Line separator, <220> field identifier
L:347 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:23, <213>
ORGANISM:Artificial Sequence
L:347 M:283 W: Missing Blank Line separator, <400> field identifier
L:347 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:347
L:354 M:283 W: Missing Blank Line separator, <220> field identifier
L:355 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:24, <213>

ORGANISM:Artificial Sequence

L:355 M:283 W: Missing Blank Line separator, <400> field identifier

L:355 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:24,Line#:355

L:362 M:283 W: Missing Blank Line separator, <220> field identifier

L:363 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:25, <213>

ORGANISM:Artificial Sequence

VERIFICATION SUMMARY

DATE: 05/22/2006

PATENT APPLICATION: US/10/578,840

TIME: 14:19:21

Input Set : A:\060641-0113sequencetext.txt

Output Set: N:\CRF4\05222006\J578840.raw

L:363 M:283 W: Missing Blank Line separator, <400> field identifier
L:363 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:25,Line#:363
L:370 M:283 W: Missing Blank Line separator, <220> field identifier
L:371 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:26, <213>
ORGANISM:Artificial Sequence
L:371 M:283 W: Missing Blank Line separator, <400> field identifier
L:371 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:371
L:378 M:283 W: Missing Blank Line separator, <220> field identifier
L:379 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:27, <213>
ORGANISM:Artificial Sequence
L:379 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:379
L:387 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:28, <213>
ORGANISM:Artificial Sequence
L:387 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:28,Line#:387
L:395 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:29, <213>
ORGANISM:Artificial Sequence
L:395 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:29,Line#:395
L:406 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:30
L:408 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:30
L:436 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:31, <213>
ORGANISM:Artificial Sequence
L:436 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:31,Line#:436
L:446 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:130, <213>
ORGANISM:Artificial Sequence
L:446 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:32
differs:130
L:446 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:32,Line#:446
L:476 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:35
differs:23
L:477 M:254 E: No. of Bases conflict, LENGTH:Input:23 Counted:22 SEQ:35
L:477 M:252 E: No. of Seq. differs, <211> LENGTH:Input:23 Found:22 SEQ:35
L:484 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:36
differs:23
L:489 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for
SEQ ID#:37
L:490 M:206 E: Mandatory field data missing, <213> ORGANISM
L:544 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:40
L:546 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:40
L:593 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:43
L:595 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:43
L:642 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:46
L:644 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:46
L:691 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:49
L:693 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:49
L:740 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52
L:742 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:52
L:778 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:54
differs:5
L:805 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:57
L:807 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:57
L:886 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:64
L:888 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:64
L:935 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:67

L:937 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:67
L:966 M:254 E: No. of Bases conflict, LENGTH:Input:24 Counted:25 SEQ:68
L:966 M:252 E: No. of Seq. differs, <211> LENGTH:Input:24 Found:25 SEQ:68
L:990 M:254 E: No. of Bases conflict, LENGTH:Input:45 Counted:46 SEQ:71
L:990 M:252 E: No. of Seq. differs, <211> LENGTH:Input:45 Found:46 SEQ:71
L:995 M:206 E: Mandatory field data missing, <213> ORGANISM
L:1009 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:73

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L:1011 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:73
L:1063 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:74
L:1065 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:74
L:1128 M:206 E: Mandatory field data missing, <213> ORGANISM
L:1142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:78
L:1144 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:78
L:1244 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:79
L:1246 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:79
L:1324 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:79
L:1327 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:79
L:1401 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:87
L:1409 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:37 SEQ:88
L:1415 M:206 E: Mandatory field data missing, <213> ORGANISM
L:1428 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:708 SEQ:89
L:1433 M:206 E: Mandatory field data missing, <213> ORGANISM
L:1469 M:206 E: Mandatory field data missing, <213> ORGANISM
L:1482 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:708 SEQ:91
L:1487 M:206 E: Mandatory field data missing, <213> ORGANISM
L:1523 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:92